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Title:
Perfect score:
Sequence:
                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                               Database :
                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                           Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OM protein - protein search, using sw model
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PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Gapop 10.0 , Gapext 0.5
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1284
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	G	4	ω	2	_	No.	Result
91	92	92.5	92.5	94	94	94	95	96.5	98	99.5	103	103.5	103.5	104	107	108	110	110.5	114.5	118	146	146	164	171	869.5	875.5	877.5	1060	Score	
7.1	7.2	7.2	7.2	7.3	7.3	7.3	7.4	7.5	7.6	7.7	8.0	8.1	8.1			8.4		8.6	8.9	9.2	11.4	11.4	12.8	13.3	67.7	68.2	68.3	82.6	Match Length	Operv
284	2594	638	279	1825	1825	468	814	378	897	638	638	830	677	616	608	281	831	634	522	581	635	579	626	625	507	265	507	508	Length [	
2	Ν	N	N	N	Ν	N	N	Ŋ	ר	N	N	2	N	N	N	1	N	N	N	N	N	N	N	Ν	1	2	1	1	DB	
S27931	A35774	A33505	в32985	T32828	C88400	A45268	AE2051	A40266	A39255	B28176	S12136	I50455	S33608	A30304	S32823	RGBYA2	JQ1655	S33339	B45268	145971	A45266	B45266	S37622	S35317	A32385	S14081	A46713	ZUHUR	ID	
Env/v-mpl fusion p	kinase-related pro	somatotropin recep	somatotropin-bindi	hypothetical prote		interleukin-9 rece	endopeptidase Clp	interleukin-3 rece	cytokine receptor	somatotropin recep	somatotropin recep	prolactin receptor	somatotropin-bindi	prolactin receptor	somatotropin recep	amino acid biosynt	prolactin receptor	somatotropin recep	interleukin-9 rece	prolactin receptor	MPL-P protein prec	MPL-K protein prec	proto-oncogene - m	iO.		erythropoietin rec	erythropoietin rec	erythropoietin rec	Description	

5	44	43	42	41	40	39	38	37	36	35	34	S S	32	31	30
86.5	87	87	87	87	88	88	88	88	88.5	90	90	90	91	91	91
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F70019	A36116	A34631	A41070	A29884	A43254	A40144	A59405	B59405	A37803	н69879	KIBYHA	I56896	I53269	177524	177525
nifS protein homol	prolactin receptor	lactogen receptor	prolactin receptor	prolactin receptor	protein-tyrosine-p	prolactin receptor	prolactin receptor	prolactin receptor	beta-fructofuranos	ATP-dependent DNA	hexokinase (EC 2.7	gene gfi-2 protein	prolactin receptor	prolactin receptor	prolactin receptor

## ALIGNMENTS

A;Accession: A55280 A;Molecule type: DNA A;Residues: 1-17;381-387, 'LLEQQQDA',391-395;504-508 <pen> A;Residues: 1-17;381-387, 'LLEQQQDA',391-395;504-508 <pen> A;Note: sequence modified after extraction from NCBI backbone A;Note: the authors translated the codon GAT for residue 31 as B A;Note: an insert compared to other published sequences is considered by authors as 1 R;Maouche, L; Tournamille, C.; Hattab, C.; Boffa, G.; Cartron, J.P.; Chretien, S. Blood 78, 2557-2563, 1991 A;Title: Cloning of the gene encoding the human erythropoietin receptor.</pen></pen>	Exp. Hematol, N., 51, 3011, 1.1  Exp. Hematol, 19, 973-977, 1991  A; Pitle: The erythropoletin receptor gene: cloning and identification of multiple tra A; Reference number: A53958; MUID:91372359  A; Accession: A53958  A; Molecule type: mRNA  A; Residues: 1-908 < EHR> A; Renny, L.A.; Forget, B.G. Genomics 11, 974-980, 1991  A; Fitle: Genomic organization of the human erythropoietin receptor gene. A; Reference number: A55280; MUID:92147143	A;Status: not compared with conceptual translation A;Molecule type: mRNA; DNA A;Molecule type: mRNA; DNA A;Residues: 1-101, 'K', '103-188, 'RP', 191-243, 'E', '245-508 <win> R;Noguchi, C.T.; Bae, K.S.; Chin, K.; Wada, Y.; Schechter, A.N.; Hankins, W.D. Blood 78, 2548-2556, 1991 A;Title: Cloning of the human erythropoietin receptor gene. A;Reference number: A49824 A;Recession: A49824 A;Recession: A49824 A;Molecule type: DNA A;Residues: 1-508 <nog> A;Cross-references: GB:S45332; NID:9255496; PIDN:AAB23271.1; PID:g255497 A;Experimental source: placenta A;Note: sequence extracted from NCBI backbone (NCBIN:113293, NCBIP:113294) B;Bybraman K : St Tohn T</nog></win>	C;Accession: A43799; A60160; A49824; A5328; A5280; I52563 R;Jones, S.S.; D'Andrea, A.D.; Haines, L.L.; Wong, G.G. Blood 76, 31-35, 1990 A;Title: Human erythropoietin receptor: Cloning, expression, and biologic characteriz A;Reference number: A43799; MUID:90304340 A;Reference number: A43799; MUID:90304340 A;Accession: A43799 A;Molecule type: mRNA A;Residues: 1508 < JONY A;Cross-references: GB:M60459; NID:g182244; PIDN:AAA52403.1; PID:g182245 R;Winkelmann, J.C.; Penny, L.A.; Deaven, L.L.; Forget, B.G.; Jenkins, R.B. Blood 76, 24-30, 1990 A;Reference number: A60160; MUID:90304334 A;Accession: A60160	RESULT 1  ZUHUR erythropoietin receptor precursor - human C;Species: Homo sapiens (man) C;Species: 12-Feb-1993 #sequence revision 05-Apr-1995 #text change 22-Jun-1999 C;Date: 12-Feb-1993 #sequence revision 05-Apr-1995 #text change 22-Jun-1999

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A; Reference number: 152563; MUID:92399734
A; Accession: 152563
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-96 <RESS
A; Cross-references: GB:M76595; NID:9182147; PIDN:AAA52393.1; PID:955326
C; Genetics:
C; Genetics:
A; Gene: GDB:EPOR
A; Cross-references: GDB:125242; OMIM:133171
A; Map position: 19p13.3-19p13.2
A; Introns: 39/1; 84/2; 143/1; 195/3; 247/1; 276/2; 305/3
C; Superfamily: erythropoietin receptor; cytokine receptor homology
C; Keywords: alternative splicing; cytokine receptor; glycoprotein; transferences: signal sequence #status predicted <SIG>F; 25-508/Product: erythropoietin receptor #status predicted <MAT>F; 52-239/Domain: cytokine receptor homology <CRS>
F; 233-237/Region: WSXWS motif
F; 231-272/Domain: transmembrane #status predicted <TMM>F; 25-62,91-107/Disulfide bonds: #status predicted <TMM>F; 25-250/Disulfide Billows #status P
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11; Mismatches
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C;Superiamily: C; C;Keywords: cytokine receptor; transmum-
C;Keywords: cytokine receptor homology
F;52-238/Domain: cytokine receptor homology
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C;Date: 18-Fab-1994 #sequence_revision
C;Accession: S14081; 149653
R;Kuramochi, S.; Ikawa, Y.; Todokoro, K
J. Mol. Biol. 216, 567-575, 1990
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A; Residues: 1-24 <RES>
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A; Accession: I49653
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J. Biol. Chem. 266, 6952-6956, 1991
A;Title: Spleen focus-forming virus long terminal
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A; Residues: 1-265 < KUR>
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RESULT A32385

erythropoietin

receptor

precursor,

membrane-bound

form

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C;Species: Mus musculus (house mouse)
C;Date: 28-Sep-1990 #sequence_revision 05-Apr-1995 #text_change 22-Jun-1999
C;Accession: A41686; A32385; S13249
R;Hino, M.; TOjo, A.; Misawa, Y.; Morii, H.; Takaku, F.; Shibuya, M.
Mol. Cell. Biol. 11, 5527-5532, 1991
A;Title: Unregulated expression of the erythropoietin receptor gene caused k A;Reference number: A41686; MUID:92017832
A;Accession: A41686
A;Molecule type: mRNA
A;Residues: 1-507 <HIN>
A;Coss-references: GB:S59388; NID:9237036; PIDN:AAB20029.1; PID:9237037
A;Experimental source: murine erythroleukemia (MEL) cell line F5-5
R;D Andrea, A.D.; Lodish, H.F.; Wong, G.G.
Cell 57, 277-285, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: erythropoletin receptor; cytokine receptor homology c;Keywords: alternative splicing; cytokine receptor; glycoprotein; F;1-24/Domain: signal sequence #status predicted <SIG>F;25-507/Product: erythropoletin receptor #status predicted <MAT>F;25-249/Domain: extracellular #status predicted <EXT>F;25-238/Domain: cytokine receptor homology <CRS>F;250-271/Domain: transmembrane #status predicted <INT>F;27-2507/Domain: intracellular #status predicted <INT>F;27-507/Domain: intracellular #status predicted F;37-501-105/Disulfide bonds: #status predicted F;52-62,90-106/Disulfide bonds: #status predicted F;57-Binding site: carbohydrate (Asn) (covalent) #status predicted
         C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: S35317; S35316
R;Skoda, R.C.; Seldin, D.C.; Chiang, M.K.; Peichel, C.L.; Vogt, T.F.; Leder,
                                                                                                                                                                                                                                                                                                                                           Qy
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A;Accession: S13249
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A;Experimental source: murine erythroleukemia (MEL) cells, subclone 745
R;Kuramochi, S.; Tlawa, Y.; Todokoro, K.
J. Mol. Biol. 216, 567-575, 1990
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A;Accession: A32385
A;Molecule type: mRNA
A;Residues: 1-507 <DAA>
A;Residues: 1-507 <DAA>
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A; Residues: 1-507 < KUR>
                                                                                                                                        hematopoietic growth factor receptor precursor -
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                                                                                                                                                                                                                                                                                                                                                                                                           RRAEEGSHVVLRWLPPPGAPMTTHIRYEVDVSAGNRAGGTQRVEVLEGRTECVLSNLRGG
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2645-2653,
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D.C.; Chiang, M.K.;
1993
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A;Accession: S35316
A;Molecule type: DNA
A;Residues: 1-70 <SKW>
A;Residues: 1-70 <SKW>
A;Cross references: EMBL:Z22657
A;Cross references: EMBL:Z22657
C;Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane
E;1-25/Domain: signal sequence #status predicted <SIG>
F;26-625/Product: hematopoletic growth factor receptor #status predicted <MAT>
E;261-265/Region: WGXMS motif
E;261-265/Region: WGXMS motif
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                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-626 <VIG>
A;Cross-references: EMBL:X73677; NID:g404318; PIDN:CAA52031.1; PID:g404319
                                                                                                                                                                                                                                       A; Reference number: S. A; Accession: S37622
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                  proto-oncogene - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: S37622
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A;Accession: S35317
A;Molecule type: mRNA
A;Residues: 1-625 <SKO>
A;Cross-references: EMBL:Z22649; NID:g394725; PIDN:CAA80365.1; PID:g394726
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18
                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                        I.; Florindo, C.; Fichelson, S.; Guenet, J.L.;
8, 2607-2615, 1993
Characterization of the murine Mpl proto-oncoge
                                     SKAALLAARGPEELLCFTERLEDLVCFFEEAASAGVGPGNFSFSFQLEDEPWKLCRLHQA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GFWSAWSEPVSL
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SQDVFLLALGTEPLNCFSQTFEDLTCFWDEEEAA--PSGTYQLLYAYRGEKPRACPLYSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SQDVFLLALGTEPLNCFSQTFEDLTCFWDEEEAA--PSGTYQLLYAYRGEKPRACPLYSQ
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                                                                                 Conservative
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                                                                               34;
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                                                                          Score 164; DB 2;
Pred. No. 2.6e-06;
4; Mismatches 105
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No. 6.4e-07;
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) (covalent) #status
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δõ

64

PTARGAIRFWCSLPT-ADTSSFYPLELRLTAAS-GAPRFHRVIHINEVVLLDAPVGLVAR 121

C; Keywords: transmembrane

protein

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MPL-K protein precurs
C;Species: Homo sapie
C;Date: 27 Jun-1994
C;Accession: B45266
R;Vigon, I; Mornon,
Proc. Natl. Acad. Sci
                                          R;Vigon, I.; Mornon, J.P.; Cocault, L.; Mitjavila, M.T.; Proc. Natl. Acad. Sci. U.S.A. 89, 5640-5644, 1992
A;Title: Molecular cloning and characterization of MPL, t A;Reference number: A45266; MUID:92302297
A;Accession: A4526
A;Status: preliminary
A,Status: preliminary
                                                                                                                             R:Vigon, I.; Mornon, J.P.; Cocault, L.; Mitjavila, M.T.

Proc. Natl. Acad. Sci. U.S.A. 89, 5640-5644, 1992

A:Title: Molecular cloning and characterization of MPL,

A:Reference number: A45266; MUID:92302297

A:Accession: B45266

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-579 < VIG>

A:Cross-references: GB:M90103; NID:g184262; PIDN:AAA6997
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A; Molecule type: mRNĀ
A; Residues: 1-635 <VIG>
A; Cross-references: GB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVPTFGTRYVCQFPAQVEVRLFFPLHLWVKNVSLNQTLIQRVLFVDSVGLPAPPRVIKAR
                                                                                                                                                                                                                                                                                                              MAEPSFGGFWSAWSEPVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                LADESGHVVIRW-LPPPETPMTSHIRFEL----DISAGNGAGSVQRVE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QPDGVSLRGSWGPWSFPVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RMAEPSFGGFWSAWSEPVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MPNPVPVLDQPPCVHPTASQPHGPVRTSPAGEAPFLTVKGGSCLVSGLQASKSYWLQLRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGSQPGELQIHWEAPAPE--ISDFLRHELRYGPTDSSNATAPSV--IQLLSTETCCPTLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LADESGHVVIRW-LPPPETPMTSHIRFELDI----SAGNGAGSVQRVELLEGRT-----
                                                                                                                                                                                                                                                                                 PDGISLGGSWGSWSLPVTV
                                                                                                                                                                                                                                                                                                                                               HSASALDQSPCAQPTMPWQDGPKQTSPSREASALTAEGGS-CLISGLQPGNSYWLQLRSE
                                                                                                                                                                                                                                                                                                                                                                                                               GGSQPGELQISWEEPAPE--ISDFLRYELRYGPRDPKNSTGPTVIQLIATETCCPALQRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMPHFGTRYVCQFPDQEEVRLFFPLHLWVKNVFLNQTRTQRVLFVDSVGLPAPPSIIKAM 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTARGAIRFWCSLP-TADTSSFVPLELRL-TAASGAPRFHRVIHINEVVLLDAPVGLVAR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SQDVSLLASDSEPLKCFSRTFEDLTCFWDEEEAAPSGTYQLLYAYPRE-KP-RACPLSSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          precursor - human (fragment)
mo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
 GB:M90102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #sequence_revision 27-Jun-1994 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.4%;
22.8%;
                                                                                                                                                                                                                                                                                 278
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 NID: g184260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 146; DB 2;
Pred. No. 8.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitjavila, M.T.; Tambourin,
5644, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIDN: AAA69972.1;
   PIDN: AAA69971.1;
                                                                                                                                                                                                                                                                                                                                                                               LLEGRTECVLSNLRGRTRITIAVRAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107;
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                                                                                                  the human homolog of the v-mpl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the human homolog of the v-mpl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PID:g184263
 PID:g184261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P.; Gisselbrecht,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                  Gisselbrecht,
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 RESULT 10
B45268
interleukin-9
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prolactin receptor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change
C;Accession: I45971
C;Accession: I45971 M.A.; Schuler, L.A.
                                                                                                                                                                                                                                                                                                                                  A;Gene: PRLR
C;Superfamily: c
F;36-221/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mol. Cell. Endocrinol. 89, 47-58, 1992
A; Title: Molecular cloning of the bovine prolactin
A; Reference number: I45971; MUID:93246019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Вb
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-581 <SCO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: I45971
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Best Local
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Best Local Similarity
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                               171 ECVLSNLRGRTRITIAVRARMAEPSFGGFWSAWSEPVSL
 190
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                                                                                                                             75 CPDYKTGGPNSCYFSKKHTSIWKMYVITVNAINQMGISSSDPLY---VHVTYIVEPEPPA
                                                                                                                                                          63
                                                                                                                                                                                        20
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                                                                                                                                                                                                            SLLNGQSPPEKPKLVKCRSPGKETFTCWWEPGADGGL-PTNYTLTYHKEGE----TLIHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDGISLGGSWGSWSLPVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGSQPGELQISWEEPAPE--ISDFLRYELRYGPRDPKNSTGPTVIQLIATETCCPALQRP
QLKIFNLYPGQKYLVQIRCK---PDH-GYWSEWSPESSI
                                                            NLTLELKHPEDRKPYLWIKWSPPTMTDVKSGWFIIQYEIRLKPEKATDWETHFTLKQ--T
                                                                                            GLVARL---ADESGHVVIRWLPPPETPMTSH----IRFELDISAGNGAGSVQRVELLEGRT 170
                                                                                                                                                            APTARGAIRFWCSLPTADTSSFVPLELRLTA-----ASGAPRFHRVIHINEVVLLDAPV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAEPSFGGFWSAWSEPVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                {\tt HSASALDQSPCAQPTMPWQDGPKQTSPSREASALTAEGGS-CLISGLQPGNSYWLQLRSE}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMPHFGTRYVCQFPDQEEVRLFFPLHLWVKNVFLNQTRTQRVLFVDSVGLPAPPSIIKAM 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTARGAIRFWCSLP-TADTSSFVPLELRL-TAASGAPRFHRVIHINEVVLLDAPVGLVAR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        {\tt SQDVSLLASDSEPLKCFSRTFEDLTCFWDEEEAAPSGTYQLLYAYPRE-KP-RACPLSSQ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SKAALLAARGPEELLCFTERLEDLVCFFEEAASAGVGPGNFSFSFQLEDEPWKLCRLHQA
                                                                                                                                                                                                                                                        48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                  cytokine receptor homology n: cytokine receptor homology
                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                               GB:L02549; NID:g163617;
                                                                                                                                                                                                                                                                    9.2%;
21.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.4%; Score 146; DB 2; 22.8%; Pred. No. 9.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35;
                                                                                                                                                                                                                                                        40;
                                                                                                                                                                                                                                                                    Score 118;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                    homology
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                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -DISAGNGAGSVQRVE---
                                                                                                                                                                                                                                                                                                                                                                                                  PIDN:AAA51417.1;
                                                                                                                                                                                                                                                                                                                                     <CRS>
                                                                                                                                                                                                                                                                       .024;
                                                                                                                                                                                                                                                                                    DB 2;
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                                                                                                                                                                                                                                                        101;
                                  209
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receptor

precursor

human

KWEPPPNT

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R:Adams, T.E.; Baker, L.; Fiddes, R.J.; Brandon, M.R. Mol. Cell. Endocrinol. 73, 135-145, 1990
A:Title: The sheep growth hormone receptor: molecular A:Reference number: S33339; MUID:91099608
A:Accession: S33339
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                                                                 Qy
                                                                                                        В
                                                                                                                                      QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                            somatotropin receptor - sheep
N;Alternate names: growth hormone receptor
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 08-Dec-1993 *sequence_revision 01-Dec-1995 *text_change 08-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QY
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A;Title: Expression cloning of the murine and human interleukin 9 receptor cDNAs. A; Reference number: A45268; MUID:92302307
A; Accession: B45268
A; Status: preliminary
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-522 <RENN
A; Cross-references: GB:M84747; NID:g184508; PIDN:AAA58679.1; PID:g184509
C; Keywords: glycoprotein; receptor; T-cell proliferation; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Species: Homo sapiens (man) C; Date: 27-Jun-1994 #sequence_C; Accession: B45268 R; Renauld, J.C.; Druez, C.; Ke Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:M82912; NID:g165888; PIDN:AAA73171.1; C;Superfamily: fibronectin type III repeat homology
                                                                                                                                                                                                                                                                                                          A; Residues: 1-634 < ADA>
                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: S33339
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Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 05-Nov-1999
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Best Local
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   132
                                     111
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                                                                                                                            19 CFTERLEDLYCFFEEAASAGY-GPGNFS-FSFQLEDEPWKLCRLHQAPTARGAIRFWCSL
                                                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 22.
                                                                                                        CRSPELETFSCHWTDGANHSLQSPGSVQMFYIRRDIQEWKEC - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDLQSNIS--SGHCILTWSISPALEPMTTLLSYELAFKKQEEAWEQAQHRDHIVGVTWLI 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VGLVARLADESGHVVIRW-LPPPETPMTSHIRFELDISAGNGA-GSVQRVELLEGRTECV 173
 RWLPPPET
                                   NSSYTSVWTPYCIKLTSNGGIVD-HKCFSVEDIVQPDPPVGLNWTLLNISLTEIHADILV
                                                                     PTADTSSFVPLELRLTAASGAPRFHRVIHINEVVLLDAPVGLVARLADES-----GHVVI 131
                                                                                                                                                                                                                                                                                                                                            preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPGNTLVAVSIFLLLTGPTYLLFKLSPRVKRIFYQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----CILRGSECTVVLPPEAVLVPSDNFTITFHHCMSGREQVSLVDPEYLPRRHVKLDPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QGPRSRTFTCLTNNILRIDCHW-SAPELGQG-----SSPWLLFTSNQAPGGTHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RGPEE--LLCFTERLEDLVCFFEEAASAGVGPGNFSFSFQLEDEPWKLCRLHQAPTARGA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEAFELDPGFIHEARLRVQMATLEDDVVEEERYTGQWSEWSQPVCFQAPQRQGPLIPPWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IRFWCSLPTADTSSFVPLELRLTAASG-APRFHRVIHINEV-----
                                                                                                                                                                                                Similarity
                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---RGRTRITIAVRAR--MAEPSFGGFWSAWSEPVS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -LLTGGGGSRMEKLEQKVKELLRKN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.; Kermouni,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.9%; 5-
22.1%; Pre
                                                                                                                                                                                              8.6%;
26.6%;
                                                                                                                                                                               24;
                                                                                                                                                                                          Score 110.5; D
Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 114.5; DB 2;
Pred. No. 0.042;
2; Mismatches 110;
                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Houssiau,
                                                                                                                                                                                                                                                                                                                                                                                            molecular cloning
                                                                                                                                                                                                               DB
                                                                                                                                                                             57;
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                                                                                                                                                                           Indels
                                                                                                                                                                                                             Length
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                                                                                                        -PDYVSAGENSCYF 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             522;
                                                                                                                                                                                                                                                                                                                                                                                            and ontogeny of mRNA expre
                                                                                                                                                                                                                                                                                    PID:g165889
                                                                                                                                                                           13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -VLLDAP 115
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                                                                                                                                                                           Gaps
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                                 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
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A; Experimental source: kidney
C; Superfamily: cytokine receptor homology
C; Keywords: glycoprotein; transmembrane protein
F; 1-23/Domain: signal sequence #status predicted <SIG>
F; 24-831/Product: prolactin receptor #status predicted
F; 36-219/Domain: cytokine receptor homology <CRS1>
                                                                                                  R;Dietrich, F.S. submitted to the EMBL Data Library, December 1994 submitted to the EMBL Data Library, December 1994 A;Description: Saccharomyces cerevisiae chromosome A:Reference number: S50428
                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 81, 6442-6446, 19
A; Title: Evidence for translational regulation
A; Reference number: A03605; MUID:85038531
                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Saccharomyces cerevisiae
C;Date: 27-Nov-1985 #sequence_revision
C;Accession: A03605; S50450; A03604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;239-425/Domain: cytokine receptor homology <CRS2>
F;439-462/Domain: transmembrane #status predicted <TMM>
F;59,91,100,112,132,262,303,315,335,647,701,800/Binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima
Biochem. Biophys. Res. Commun. 188, 490-496,
A;Title: Double antenna structure of chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prolactin receptor precursor - chicken
C; Species: Gallus gallus (chicken)
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 28-Jul-2000
                                               A; Molecule type: DNA
A; Residues: 1-281 <DIE>
                                                                                           A; Reference number: A; Accession: S50450
                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-281 <HIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-831 <TAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A; Accession: JQ1655
A;Cross-references: EMBL:U18530; NID:g602367; R;Thireos, G.; Penn, M.D.; Greer, H.
                                                                                                                                                                                                          A;Cross-references: EMBL:K02205; NID:g171581; PIDN:AAA34640.1;
                                                                                                                                                                                                                                                                            A; Accession: A03605
                                                                                                                                                                                                                                                                                                                                                                R; Hinnebusch, A.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid biosynthesis regulatory
N; Alternate names: protein YEL009c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: DDBJ:D13154; NID:g222848; PIDN:BAA02439.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: JQ1655
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 PEELLCFTERLEDLVCFFEEAASAGVGPGNFSFSFQLEDEPWKLCRLHQAPTARGAIRFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLSNLRGRTRITIAVRARMAEPSFGGFWSAWSEPVSLLTGGGGSRMEK 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMYLWAKWSPPLLADASSNHLYHYELRIKPEEKEEWETISVG-----VQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --HVVIRWLPPPETPMTSH--IRFEL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYFNKNHTSPWTTFNITVTATNEIGSNSSDPQY---VDVTSIVQPGSPVNLTLETKRSAN 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CSLPTADTSSFVPLELRLTAA-----SGAPRFHRVIHINEVVLLDAPVGLVARLADESG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PKIIRCRSLEKETFSCWWKPGSDGGL-PTNYTLFYSKDSEE----EIYECPDYRTSGPNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KINRLNAGMRYVVQVRCTL-DP---GEWSEWSSERHILIPSGQSPPEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.5%;
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                         PIDN: AAB64486.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                                        the
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                                                                                                                                      V cosmids
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                                                                                                                                          9871,
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                       PID:g602376;
                                                                                                                                                                                                          PID:g171584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46;
                                                                                                                                                                                                                                                                                                                                                                                                               21-Jul-2000
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                                                                                                                                          8199,
                                                                                                                                                                                                                                                                                                                        general amino
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                                                                                                                                          9867,
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                            GSPDB:GN0
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                                                                                                                                          9495
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A; Accession: A03604
A; Molecule type: DNA
A; Residues: 1-238, 'PG'
A; Cross-references: E
C; Genetics:
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A; Title: 5'
A; Reference
                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: A49812; MUID:94158898
A; Accession: A49812
A; Status: preliminary
A; Molecule type: mRNA
A; Rosidues: 1-109 <HUA>
A; Cross references: GB:568576; NID:9499137; PIDN:AAB29983.1; PID:9499138
A; Experimental source: liver, normal chicken
A; Note: this truncated form is a minor splice form in normal chickens and the compact of the control of the co
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A;Cross-references: SGD:S0000735; MIPS:YEL009c
A;Map position: 5L
C;Function:
A;Description: transcription regulation
A;Note: regulared under amino acid starvation conditions for increasing the transcription
C;Superfamily: amino-acid biosynthesis regulatory protein; fos/jun DNA-binding domain hc
C;Keywords: DNA binding; leucine zipper; transcription regulation
F;220-260/Domain: fos/jun DNA-binding domain homology <FJD>
F;253-281/Region: leucine zipper motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Molecular cloning of the chicken growth hormone receptor complement A;Reference number: S32823; MUID:91243665
A;Accession: S32823
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-608 <BUR>
A;Residues: 1-608 <BUR>
A;Residues: 1-608 <BUR>
A;Residues: N:Cogburn, L.A.; Agarwal, S.K.; Marks, H.L.; Burnside, J.
Mol. Endocrinol. 7, 1391-1398, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Burnside, J.; Llou, J., 1991
R;Burnside, J.; Llou, J., 1991
Endocrinology 128, 3183-3192, 1991
A;Title: Molecular cloning of the chicken
A;Title: S32823; MUID:91243665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N;Contains: somatotropin receptor, short form C;Specles: Gallus gallus (chicken) C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 C;Accession: S32823; A49812 R;Burnside, J.; Liou, S.S.; Cogburn, L.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N; Alternate names: growth hormone receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
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Best Local S
Matches 23
                                                                                                                                                                                                                                                         Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               249
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AIRFWCSLPTADTSSFVPLELRLTAASGAPRFHRVIHINEVVLLDAPVGLVARLADES--
                                                                               PQISKCRSPELETFSCYWTD-----GKVTTSGTIQLLYMKRSDEDWKEC-----PDYIT
                                                                                                                                                   PEELLCFTERLEDLVCFFEEAASAGVGPGNFSFSFQL----EDEPWKLCRLHQAPTARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RMKQLEDKVEELLSKNYHLENEVARLKKLVGER 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1-238, 'PGVLVRESCKE'
                                                                                                                                                                                                                       Similarity 26.7
54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                       Score 107; DB
Pred. No. 0.23
26; Mismatches
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Pred. No. 0.
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.072;
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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 41-58,'X',60-66;90-93,'X',95-96,'X',98-103,'X',105,'NX',108;150-164,'XX'
A; Note: the amino end of the mature protein was blocked
C; Superfamily: cytokine receptor homology
C; Keywords: blocked amino end; 91ycoprotein; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>F;25-616/Product: prolactin receptor 2 #status predicted <MANT>F;36-221/Domain: cytokine receptor homology CCRS>F;36-221/Domain: transmembrane #status predicted <MMN>F;35-258/Domain: transmembrane #status predicted <MMN>F;59,104,132,347,389,411/Binding site: carbohydrate (Asn) (covalent) #status predict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross references: GB:J04510; NID:g165669; R;Waters, M.J.; Spencer, S.A.; Hamlin, G.; Int. J. Biochem. 22, 1089-1095, 1990 A;Title: Purification and partial sequence (A;Reference number: A60380; MUID:91146782 A;Accession: A60380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prolactin receptor 2 precursor - rabbit
W;Alternate names: prolactin receptor, mammary gland
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Jul-2000
C;Accession: A30304; A60380
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A; Residues: 1-616 <EDE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Edery, M.; Jolicoeur, C.; Levi-Meyrueis, C. proc. Natl. Acad. Sci. U.S.A. 86, 2112-2116,
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                                                                                                                                    ---VARLADESGHVVIRWLPPPETPMTS---HIRFELDISAGNGAGSVQRVELLEGRTEC
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21.2%;
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Search completed: Job time: 390 sec August 28, 2002,

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